



SEQUENCE LISTING

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<120> NUCLEIC ACID MOLECULE ENCODING A (POLY)PEPTIDE CO-SEGREGATING IN MUTATED
FORM WITH AUTOIMMUNE POLYENDOCRINOPATHY CANDIDIASIS ECTODERMAL DYSTROPHY (APECED)

<130> VOSS1130

<140> US 09/509,595

<141> 2000-07-05

<150> EP 97117154.1

<151> 1997-10-02

<150> EP 97117398.4

<151> 1997-10-08

<150> EP 97119810.6

<151> 1997-11-12

<160> 30

<170> PatentIn version 3.0

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<211> 2245

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (121)..(1758)

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atg gcg acg gac gcg gcg cta cgc cgg ctt ctg agg ctg cac cgc acg 168

Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg Thr
1 5 10 15

gag atc gcg gtg gcc gtg gac agc gcc ttc cca ctg ctg cac gcg ctg 216

Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu Leu His Ala Leu
20 25 30

gct gac cac gac gtg gtc ccc gag gac aag ttt cag gag acg ctt cat 264

Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His
35 40 45

ctg aag gaa aag gag ggc tgc ccc cag gcc ttc cac gcc ctc ctg tcc 312

Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser

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tgg ctg ctg acc Trp Leu Leu Thr 65	cag gac tcc Gln Asp Ser 70	aca gcc atc Thr Ala Ile 75	ctg gac ttc Leu Asp Phe 80
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ctg ttc aag gac Leu Phe Lys Asp 85	tac aac ctg Tyr Asn Leu 90	gag cgc tat Glu Arg Tyr 95	ggc cgg ctg Gly Arg Leu 100
408			
ctg gac agc ttc Leu Asp Ser Phe 100	ccc aaa gat Pro Lys Asp 105	gtg gac ctc Val Asp Leu 110	agc cag ccc Ser Gln Pro 115
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agg aag ccc ccg Arg Lys Pro Pro 115	gcc gtc ccc Ala Val Pro 120	aag gct ttg Lys Ala Leu 125	gta ccg cca Val Pro Pro 130
504			
ccc acc aag agg Pro Thr Lys Arg 130	aag gcc tca Lys Ala Ser 135	gaa gag gct Glu Glu Ala 140	cga gct gcc Arg Ala Ala 145
552			
gcc ctg act cca Ala Leu Thr Pro 145	agg ggc acc Arg Gly Thr 150	gcc agc cca Ala Ser Pro 155	ggc tct caa Gly Ser Gln 160
600			
aag ccc ccc aag Lys Pro Pro Lys 165	aag ccg gag Lys Pro Glu 170	agc agc gca Ser Ser Ala 175	gag cag cag Glu Gln Gln 180
648			
ctc ggg aac ggg Leu Gly Asn Gly 180	att cag acc Ile Gln Thr 185	atg tca gct Met Ser Ala 190	tca gtc cag Ser Val Gln 195
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gcc atg tcc tcc Ala Met Ser Ser 195	ggg gac gtc Gly Asp Val 200	ccg gga gcc Pro Gly Ala 205	cga ggg gcc Arg Gly Ala 210
744			
atc ctc atc cag Ile Leu Ile Gln 210	cag gtc ttt Gln Val Phe 215	gag tca ggc Glu Ser Gly 220	ggc tcc aag Gly Ser Lys 225
792			
cag gtt ggt ggg Gln Val Gly Gly 225	gag ttc tac Glu Phe Tyr 230	act ccc agc Thr Pro Ser 235	aag ttc gaa Lys Phe Glu 240
840			
agt ggg aag aac Ser Gly Lys Asn 245	aag gcc cgc Lys Ala Arg 250	agc agc agt Ser Ser Ser 255	ggc ccg aag Gly Pro Lys 260
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936			
ctg ggc cag cag Leu Gly Gln Gln 275	ggc agc gtt Gly Ser Val 280	ccc gcc cct Pro Ala Pro 285	ctg gcc ctc Leu Ala Leu 290
984			
ccc cag ctc cac Pro Gln Leu His 290	cag aag aat Gln Lys Asn 295	gag gac gag Glu Asp Glu 300	tgt gcc gtg Cys Ala Val 305
1032			

Cl
Cont.

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 Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu
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gcc tgc ctg tcc cct ccg ctc cgg gag atc ccc agt ggg acc tgg agg 1128
 Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg
 325 330 335

tgc tcc agc tgc ctg cag gca aca gtc cag gag gtg cag ccc cgg gca 1176
 Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala
 340 345 350

gag gag ccc cgg ccc cag gag cca ccc gtg gag acc ccg ctc ccc ccg 1224
 Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro
 355 360 365

ggg ctt agg tcc gcg gga gag gag gta aga ggt cca cct ggg gaa ccc 1272
 Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro
 370 375 380

cta gcc ggc atg gac acg act ctt gtc tac aag cac ctg ccg gct ccg 1320
 Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro
 385 390 395 400

cct tct gca gcc ccg ctg cca ggg ctg gac tcc tcc gcc ctg cac ccc 1368
 Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro
 405 410 415

cta ctg tgt gtg ggt cct gag ggt cag cag aac ctg gct cct ggt gcg 1416
 Leu Leu Cys Val Gly Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala
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cgt tgc ggg gtg tgc gga gat ggt acg gac gtg ctg cgg tgt act cac 1464
 Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His
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tgc gcc gct gcc ttc cac tgg cgc tgc cac ttc cca gcc ggc acc tcc 1512
 Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser
 450 455 460

cgg ccc ggg acg ggc ctg cgc tgc aga tcc tgc tca gga gac gtg acc 1560
 Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr
 465 470 475 480

cca gcc cct gtg gag ggg gtg ctg gcc ccc agc ccc gcc cgc ctg gcc 1608
 Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala
 485 490 495

cct ggg cct gcc aag gat gac act gcc agt cac gag ccc gct ctg cac 1656
 Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His
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agg gat gac ctg gag tcc ctt ctg agc gag cac acc ttc gat ggc atc 1704
 Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile
 515 520 525

ctg cag tgg gcc atc cag agc atg gcc cgt ccg gcg gcc ccc ttc ccc 1752
 Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro
 530 535 540

tcc tga cccagatgg cgggacatg cagctctgat gagagagtgc tgagaaggac 1808
 Ser
 545

acctccttcc tcagtctctgg aagccggccg gctgggatca agaaggggac agcgccac ct 1868

cttgctcagt ctcggctgta aacagctctg tgtttctggg gacaccagcc atcatgtgcc 1928

tggaattaa accctgcccc acttctctac tctggaagtc cccgggagcc tctccttgcc 1988

tggtagaccta ctataaatat aaaaattagc tgggtgtggt ggtgggtgcc tgtaatccca 2048

gtacatggg agcctgaggc atgagaatca cttgaactcg ggaggtggag gttgcagtga 2108

gtgagattg cgccactgca ctccagtctg gtcggcaaga gtgagactcc gtctcaaaaa 2168

caaaacaaaa aaaccacata acataaattt atcatctcga ccacttttca gttcagtggc 2228

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<211> 545

<212> PRT

<213> Homo sapiens

<400> 2

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 20 25 30

Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His
 35 40 45

Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser
 50 55 60

Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val
 65 70 75 80

Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile
 85 90 95

Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly
 100 105 110

Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu
 115 120 125

Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala

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Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala		
145	150	155 160
Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro		
	165	170 175
Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val		
	180	185 190
Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly		
	195	200 205
Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile		
	210	215 220
Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly		
	225	230 235 240
Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val		
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Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg		
	260	265 270
Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp		
	275	280 285
Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp		
	290	295 300
Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu		
	305	310 315 320
Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg		
	325	330 335
Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala		
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Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro		
	355	360 365
Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro		
	370	375 380

Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro
385 390 395 400

Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro
405 410 415

Leu Leu Cys Val Gly Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala
420 425 430

Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His
435 440 445

Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser
450 455 460

Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr
465 470 475 480

Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala
485 490 495

Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His
500 505 510

Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile
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Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro
530 535 540

Ser
545

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<212> DNA
<213> Murine

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ttctgttgat ctccagtcag aggctggggg 90

<210> 4
<211> 90
<212> DNA
<213> Homo sapiens

<400> 4
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ctttgttaaa cctccatgca agaggctggg 90

<210> 5
<211> 90
<212> DNA
<213> Artificial sequence

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<221> misc_feature
<222> (1)..(90)
<223> n is any nucleotide or a gap

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ntntgttnan cnnncnntnnn agnnnnnggg 90

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<213> Murine

<220>
<221> CDS
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acc gag atc gcg gtg gcc ata gac agt gcc ttt ccg ctg ctg cat gct 96
Thr Glu Ile Ala Val Ala Ile Asp Ser Ala Phe Pro Leu Leu His Ala
20 25 30
cta gcc gac cac gac gtg gtc cct gag gac aag ttc cag gag acg ctc 144
Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu
35 40 45
cgt ctg aag gag aag gaa ggc tgc ccc cag gcc ttc cac gcc ctg ctg 192
Arg Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu
50 55 60
tcc tgg ctc ctg acc cgg gac agt ggg gcc atc ctg gat ttc tgg agg 240
Ser Trp Leu Leu Thr Arg Asp Ser Gly Ala Ile Leu Asp Phe Trp Arg
65 70 75 80
att ctc ttt aag gac tac aat ctg gag cgg tac agc cgc ctg cat agc 288
Ile Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Ser Arg Leu His Ser
85 90 95
atc ctg gac ggc ttc cca aaa gat gtg gac cta aac cag tcc cgg aaa 336
Ile Leu Asp Gly Phe Pro Lys Asp Val Asp Leu Asn Gln Ser Arg Lys
100 105 110

ggg aga aag ccc ctt gct ggt ccc aag gcc gcg gta ctg cca ccc aga Gly Arg Lys Pro Leu Ala Gly Pro Lys Ala Ala Val Leu Pro Pro Arg 115 120 125	384
ccc ccc acc aag aga aaa gca ctg gag gag cct cga gcc acc cca cca Pro Pro Thr Lys Arg Lys Ala Leu Glu Glu Pro Arg Ala Thr Pro Pro 130 135 140	432
gca act ctg gcc tca aag agc gtc tcc agc cca ggc tcc cac ctg aag Ala Thr Leu Ala Ser Lys Ser Val Ser Ser Pro Gly Ser His Leu Lys 145 150 155 160	480
act aag ccc cct aag aag cca gat ggc aac ttg gag tca cag cac ctt Thr Lys Pro Pro Lys Lys Pro Asp Gly Asn Leu Glu Ser Gln His Leu 165 170 175	528
cct ctt gga aac gga att cag acc atg gca gct tct gtc cag aga gct Pro Leu Gly Asn Gly Ile Gln Thr Met Ala Ala Ser Val Gln Arg Ala 180 185 190	576
gtg acc gtg gcc tct ggg gat gtt cca gga acc cga ggg gcc gtg gaa Val Thr Val Ala Ser Gly Asp Val Pro Gly Thr Arg Gly Ala Val Glu 195 200 205	624
ggg atc ctt atc cag cag gtg ttt gag tca gga aga tcc aag aag tgc Gly Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Arg Ser Lys Lys Cys 210 215 220	672
att cag gtt ggg gga gag ttt tat aca ccc aac aag ttc gaa gac ccc Ile Gln Val Gly Gly Glu Phe Tyr Thr Pro Asn Lys Phe Glu Asp Pro 225 230 235 240	720
agt ggc aat ttg aag aac aag gcc cgg agt ggt agc agc cta aag cca Ser Gly Asn Leu Lys Asn Lys Ala Arg Ser Gly Ser Ser Leu Lys Pro 245 250 255	768
gtg gtc cga gcc aag gga gcc cag gtc act ata cct ggt aga gat gag Val Val Arg Ala Lys Gly Ala Gln Val Thr Ile Pro Gly Arg Asp Glu 260 265 270	816
cag aaa gtg ggc cag cag tgt ggg gtt cct ccc ctt cca tcc ctc ccc Gln Lys Val Gly Gln Gln Cys Gly Val Pro Pro Leu Pro Ser Leu Pro 275 280 285	864
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cag cct gag gtg tcc agg ccc ccg gag cta cct gca gag acc ccg atc	1104

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gag	ctc	aaa	gcc	agc	tct	gat	gct	gct	gtc	aca	tat	gtg	aac	ctg	ctg	1200	
Glu	Leu	Lys	Ala	Ser	Ser	Asp	Ala	Ala	Val	Thr	Tyr	Val	Asn	Leu	Leu		
	385				390					395				400			
gcc	ccg	cac	cct	gca	gct	cct	ctg	ctg	gag	cct	tca	gca	ctg	tgc	cct	1248	
Ala	Pro	His	Pro	Ala	Ala	Pro	Leu	Leu	Glu	Pro	Ser	Ala	Leu	Cys	Pro		
				405					410					415			
cta	ctg	agt	gct	ggg	aat	gag	ggg	cgg	cca	ggg	cca	gca	cca	agc	gcg	1296	
Leu	Leu	Ser	Ala	Gly	Asn	Glu	Gly	Arg	Pro	Gly	Pro	Ala	Pro	Ser	Ala		
			420					425					430				
cga	tgc	agt	gtg	tgt	ggc	gat	ggc	acc	gag	gtg	ttg	cgg	tgt	gca	cac	1344	
Arg	Cys	Ser	Val	Cys	Gly	Asp	Gly	Thr	Glu	Val	Leu	Arg	Cys	Ala	His		
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tgt	gcc	gct	gcc	ttc	cac	tgg	cgc	tgc	cac	ttc	ccg	acg	gcc	gcc	gcc	1392	
Cys	Ala	Ala	Ala	Phe	His	Trp	Arg	Cys	His	Phe	Pro	Thr	Ala	Ala	Ala		
	450					455					460						
cgg	ccg	ggg	acc	aat	ctc	cgc	tgc	aaa	tcc	tgc	tct	gca	gac	tcg	act	1440	
Arg	Pro	Gly	Thr	Asn	Leu	Arg	Cys	Lys	Ser	Cys	Ser	Ala	Asp	Ser	Thr		
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ccc	acg	cca	ggc	aca	ccg	ggc	gaa	gct	gta	ccc	acc	tct	ggg	ccc	cgt	1488	
Pro	Thr	Pro	Gly	Thr	Pro	Gly	Glu	Ala	Val	Pro	Thr	Ser	Gly	Pro	Arg		
				485				490						495			
cca	gca	cct	ggg	ctt	gcc	aag	gta	ggg	gac	gac	tct	gct	agt	cac	gac	1536	
Pro	Ala	Pro	Gly	Leu	Ala	Lys	Val	Gly	Asp	Asp	Ser	Ala	Ser	His	Asp		
			500					505					510				
cct	gtt	cta	cat	agg	gac	gac	ctg	gag	tcc	ctc	ctc	aat	gag	cac	tca	1584	
Pro	Val	Leu	His	Arg	Asp	Asp	Leu	Glu	Ser	Leu	Leu	Asn	Glu	His	Ser		
		515					520					525					
ttt	gac	ggc	atc	ctg	cag	tgg	gcc	atc	cag	agc	atg	tca	cgc	ccg	ctg	1632	
Phe	Asp	Gly	Ile	Leu	Gln	Trp	Ala	Ile	Gln	Ser	Met	Ser	Arg	Pro	Leu		
	530					535					540						
gcc	gag	aca	cca	ccc	ttc	tct	tcc									1656	
Ala	Glu	Thr	Pro	Pro	Phe	Ser	Ser										
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<210> 7
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 <212> PRT
 <213> Murine

<400> 7

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Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu
 35 40 45

Arg Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu
 50 55 60

Ser Trp Leu Leu Thr Arg Asp Ser Gly Ala Ile Leu Asp Phe Trp Arg
 65 70 75 80

Ile Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Ser Arg Leu His Ser
 85 90 95

Ile Leu Asp Gly Phe Pro Lys Asp Val Asp Leu Asn Gln Ser Arg Lys
 100 105 110

Gly Arg Lys Pro Leu Ala Gly Pro Lys Ala Ala Val Leu Pro Pro Arg
 115 120 125

Pro Pro Thr Lys Arg Lys Ala Leu Glu Glu Pro Arg Ala Thr Pro Pro
 130 135 140

Ala Thr Leu Ala Ser Lys Ser Val Ser Ser Pro Gly Ser His Leu Lys
 145 150 155 160

Thr Lys Pro Pro Lys Lys Pro Asp Gly Asn Leu Glu Ser Gln His Leu
 165 170 175

Pro Leu Gly Asn Gly Ile Gln Thr Met Ala Ala Ser Val Gln Arg Ala
 180 185 190

Val Thr Val Ala Ser Gly Asp Val Pro Gly Thr Arg Gly Ala Val Glu
 195 200 205

Gly Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Arg Ser Lys Lys Cys
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Ile Gln Val Gly Gly Glu Phe Tyr Thr Pro Asn Lys Phe Glu Asp Pro
 225 230 235 240

Ser Gly Asn Leu Lys Asn Lys Ala Arg Ser Gly Ser Ser Leu Lys Pro
 245 250 255

Val Val Arg Ala Lys Gly Ala Gln Val Thr Ile Pro Gly Arg Asp Glu
260 265 270

Gln Lys Val Gly Gln Gln Cys Gly Val Pro Pro Leu Pro Ser Leu Pro
275 280 285

Ser Glu Pro Gln Val Asn Gln Lys Asn Glu Asp Glu Cys Ala Val Cys
290 295 300

His Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe
305 310 315 320

His Leu Ala Cys Leu Ser Pro Pro Leu Gln Glu Ile Pro Ser Gly Leu
325 330 335

Trp Arg Cys Ser Cys Cys Leu Gln Gly Arg Val Gln Gln Asn Leu Ser
340 345 350

Gln Pro Glu Val Ser Arg Pro Pro Glu Leu Pro Ala Glu Thr Pro Ile
355 360 365

Leu Val Gly Leu Arg Ser Ala Ser Glu Lys Thr Arg Gly Pro Ser Arg
370 375 380

Glu Leu Lys Ala Ser Ser Asp Ala Ala Val Thr Tyr Val Asn Leu Leu
385 390 395 400

Ala Pro His Pro Ala Ala Pro Leu Leu Glu Pro Ser Ala Leu Cys Pro
405 410 415

Leu Leu Ser Ala Gly Asn Glu Gly Arg Pro Gly Pro Ala Pro Ser Ala
420 425 430

Arg Cys Ser Val Cys Gly Asp Gly Thr Glu Val Leu Arg Cys Ala His
435 440 445

Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Thr Ala Ala Ala
450 455 460

Arg Pro Gly Thr Asn Leu Arg Cys Lys Ser Cys Ser Ala Asp Ser Thr
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485 490 495

Pro Ala Pro Gly Leu Ala Lys Val Gly Asp Asp Ser Ala Ser His Asp
500 505 510

Pro Val Leu His Arg Asp Asp Leu Glu Ser Leu Leu Asn Glu His Ser
515 520 525

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Ala Glu Thr Pro Pro Phe Ser Ser
545 550

<210> 8
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<212> PRT
<213> Homo sapiens

<400> 8

Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg Thr
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20 25 30

Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His
35 40 45

Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser
50 55 60

Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val
65 70 75 80

Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile
85 90 95

Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly
100 105 110

Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu
115 120 125

Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala
130 135 140

Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala
145 150 155 160

Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro
165 170 175

Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val
180 185 190

Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly
195 200 205

Ile	Leu	Ile	Gln	Gln	Val	Phe	Glu	Ser	Gly	Gly	Ser	Lys	Lys	Cys	Ile	210	215	220	
Gln	Val	Gly	Gly	Glu	Phe	Tyr	Thr	Pro	Ser	Lys	Phe	Glu	Asp	Ser	Gly	225	230	235	240
Ser	Gly	Lys	Asn	Lys	Ala	Arg	Ser	Ser	Ser	Gly	Pro	Lys	Pro	Leu	Val	245	250	255	
Arg	Ala	Lys	Gly	Ala	Gln	Gly	Ala	Ala	Pro	Gly	Gly	Gly	Glu	Ala	Arg	260	265	270	
Leu	Gly	Gln	Gln	Gly	Ser	Val	Pro	Ala	Pro	Leu	Ala	Leu	Pro	Ser	Asp	275	280	285	
Pro	Gln	Leu	His	Gln	Lys	Asn	Glu	Asp	Glu	Cys	Ala	Val	Cys	Arg	Asp	290	295	300	
Gly	Gly	Glu	Leu	Ile	Cys	Cys	Asp	Gly	Cys	Pro	Arg	Ala	Phe	His	Leu	305	310	315	320
Ala	Cys	Leu	Ser	Pro	Pro	Leu	Arg	Glu	Ile	Pro	Ser	Gly	Thr	Trp	Arg	325	330	335	
Cys	Ser	Ser	Cys	Leu	Gln	Ala	Thr	Val	Gln	Glu	Val	Gln	Pro	Arg	Ala	340	345	350	
Glu	Glu	Pro	Arg	Pro	Gln	Glu	Pro	Pro	Val	Glu	Thr	Pro	Leu	Pro	Pro	355	360	365	
Gly	Leu	Arg	Ser	Ala	Gly	Glu	Glu	Val	Arg	Gly	Pro	Pro	Gly	Glu	Pro	370	375	380	
Leu	Ala	Gly	Met	Asp	Thr	Thr	Leu	Val	Tyr	Lys	His	Leu	Pro	Ala	Pro	385	390	395	400
Pro	Ser	Ala	Ala	Pro	Leu	Pro	Gly	Leu	Asp	Ser	Ser	Ala	Leu	His	Pro	405	410	415	
Leu	Leu	Cys	Val	Gly	Pro	Glu	Gly	Gln	Gln	Asn	Leu	Ala	Pro	Gly	Ala	420	425	430	
Arg	Cys	Gly	Val	Cys	Gly	Asp	Gly	Thr	Asp	Val	Leu	Arg	Cys	Thr	His	435	440	445	
Cys	Ala	Ala	Ala	Phe	His	Trp	Arg	Cys	His	Phe	Pro	Ala	Gly	Thr	Ser	450	455	460	
Arg	Pro	Gly	Thr	Gly	Leu	Arg	Cys	Arg	Ser	Cys	Ser	Gly	Asp	Val	Thr	465	470	475	480
Pro	Ala	Pro	Val	Glu	Gly	Val	Leu	Ala	Pro	Ser	Pro	Ala	Arg	Leu	Ala	485	490	495	
Pro	Gly	Pro	Ala	Lys	Asp	Asp	Thr	Ala	Ser	His	Glu	Pro	Ala	Leu	His	500	505	510	
Arg	Asp	Asp	Leu	Glu	Ser	Leu	Leu	Ser	Glu	His	Thr	Phe	Asp	Gly	Ile	515	520	525	

Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro
 530 535 540

Ser
 545

<210> 9
 <211> 552
 <212> PRT
 <213> Murine

<400> 9

Met Ala Gly Gly Asp Gly Met Leu Arg Arg Leu Leu Arg Leu His Arg
 1 5 10 15

Thr Glu Ile Ala Val Ala Ile Asp Ser Ala Phe Pro Leu Leu His Ala
 20 25 30

Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu
 35 40 45

Arg Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu
 50 55 60

Ser Trp Leu Leu Thr Arg Asp Ser Gly Ala Ile Leu Asp Phe Trp Arg
 65 70 75 80

Ile Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Ser Arg Leu His Ser
 85 90 95

Ile Leu Asp Gly Phe Pro Lys Asp Val Asp Leu Asn Gln Ser Arg Lys
 100 105 110

Gly Arg Lys Pro Leu Ala Gly Pro Lys Ala Ala Val Leu Pro Pro Arg
 115 120 125

Pro Pro Thr Lys Arg Lys Ala Leu Glu Glu Pro Arg Ala Thr Pro Pro
 130 135 140

Ala Thr Leu Ala Ser Lys Ser Val Ser Ser Pro Gly Ser His Leu Lys
 145 150 155 160

Thr Lys Pro Pro Lys Lys Pro Asp Gly Asn Leu Glu Ser Gln His Leu
 165 170 175

Pro Leu Gly Asn Gly Ile Gln Thr Met Ala Ala Ser Val Gln Arg Ala
 180 185 190

Val Thr Val Ala Ser Gly Asp Val Pro Gly Thr Arg Gly Ala Val Glu
 195 200 205

Gly Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Arg Ser Lys Lys Cys
 210 215 220

Ile Gln Val Gly Gly Glu Phe Tyr Thr Pro Asn Lys Phe Glu Asp Pro
 225 230 235 240

Ser Gly Asn Leu Lys Asn Lys Ala Arg Ser Gly Ser Ser Leu Lys Pro
 245 250 255

Val Val Arg Ala Lys Gly Ala Gln Val Thr Ile Pro Gly Arg Asp Glu
 260 265 270
 Gln Lys Val Gly Gln Gln Cys Gly Val Pro Pro Leu Pro Ser Leu Pro
 275 280 285
 Ser Glu Pro Gln Val Asn Gln Lys Asn Glu Asp Glu Cys Ala Val Cys
 290 295 300
 His Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe
 305 310 315 320
 His Leu Ala Cys Leu Ser Pro Pro Leu Gln Glu Ile Pro Ser Gly Leu
 325 330 335
 Trp Arg Cys Ser Cys Cys Leu Gln Gly Arg Val Gln Gln Asn Leu Ser
 340 345 350
 Gln Pro Glu Val Ser Arg Pro Pro Glu Leu Pro Ala Glu Thr Pro Ile
 355 360 365
 Leu Val Gly Leu Arg Ser Ala Ser Glu Lys Thr Arg Gly Pro Ser Arg
 370 375 380
 Glu Leu Lys Ala Ser Ser Asp Ala Ala Val Thr Tyr Val Asn Leu Leu
 385 390 395 400
 Ala Pro His Pro Ala Ala Pro Leu Leu Glu Pro Ser Ala Leu Cys Pro
 405 410 415
 Leu Leu Ser Ala Gly Asn Glu Gly Arg Pro Gly Pro Ala Pro Ser Ala
 420 425 430
 Arg Cys Ser Val Cys Gly Asp Gly Thr Glu Val Leu Arg Cys Ala His
 435 440 445
 Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Thr Ala Ala Ala
 450 455 460
 Arg Pro Gly Thr Asn Leu Arg Cys Lys Ser Cys Ser Ala Asp Ser Thr
 465 470 475 480
 Pro Thr Pro Gly Thr Pro Gly Glu Ala Val Pro Thr Ser Gly Pro Arg
 485 490 495
 Pro Ala Pro Gly Leu Ala Lys Val Gly Asp Asp Ser Ala Ser His Asp
 500 505 510
 Pro Val Leu His Arg Asp Asp Leu Glu Ser Leu Leu Asn Glu His Ser
 515 520 525
 Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Ser Arg Pro Leu
 530 535 540
 Ala Glu Thr Pro Pro Phe Ser Ser
 545 550

<210> 10

<211> 550

<212> PRT

<213> Artificial sequence

<220>

<223> Consensus sequence of SEQ ID NO.:8 and SEQ ID NO.:9

<220>

<221> VARIANT

<222> (1)..(550)

<223> Xaa denotes any amino acid

<400> 10

Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Leu	Arg	Arg	Leu	Leu	Arg	Leu	His	Arg	Thr
1				5					10					15	

Glu	Ile	Ala	Val	Ala	Xaa	Asp	Ser	Ala	Phe	Pro	Leu	Leu	His	Ala	Leu
			20					25					30		

Ala	Asp	His	Asp	Val	Val	Pro	Glu	Asp	Lys	Phe	Gln	Glu	Thr	Leu	Xaa
		35					40					45			

Leu	Lys	Glu	Lys	Glu	Gly	Cys	Pro	Gln	Ala	Phe	His	Ala	Leu	Leu	Ser
	50					55					60				

Trp	Leu	Leu	Thr	Xaa	Asp	Ser	Xaa	Ala	Ile	Leu	Asp	Phe	Trp	Arg	Xaa
65				70						75					80

Leu	Phe	Lys	Asp	Tyr	Asn	Leu	Glu	Arg	Tyr	Xaa	Arg	Leu	Xaa	Xaa	Ile
				85					90					95	

Leu	Asp	Xaa	Phe	Pro	Lys	Asp	Val	Asp	Leu	Xaa	Gln	Xaa	Arg	Lys	Gly
			100					105						110	

Arg	Lys	Pro	Xaa	Ala	Xaa	Pro	Lys	Ala	Xaa	Val	Xaa	Pro	Pro	Arg	Xaa
		115						120				125			

Pro	Thr	Lys	Arg	Lys	Ala	Xaa	Glu	Glu	Xaa	Arg	Ala	Xaa	Xaa	Pro	Ala
	130					135					140				

Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser	Pro	Gly	Ser	Xaa	Leu	Lys	Xaa
145					150					155					160

Lys	Pro	Pro	Lys	Lys	Pro	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Gln	Xaa	Leu	Pro
				165						170				175	

Leu	Gly	Asn	Gly	Ile	Gln	Thr	Met	Xaa	Ala	Ser	Val	Gln	Arg	Ala	Val
		180						185						190	

Xaa	Xaa	Xaa	Ser	Gly	Asp	Val	Pro	Gly	Xaa	Arg	Gly	Ala	Val	Glu	Gly
			195				200					205			

Ile	Leu	Ile	Gln	Gln	Val	Phe	Glu	Ser	Gly	Xaa	Ser	Lys	Lys	Cys	Ile
	210					215						220			

Gln	Val	Gly	Gly	Glu	Phe	Tyr	Thr	Pro	Xaa	Lys	Phe	Glu	Asp	Xaa	Ser
225					230					235					240

Gly	Xaa	Xaa	Lys	Asn	Lys	Ala	Arg	Ser	Xaa	Ser	Xaa	Xaa	Lys	Pro	Xaa
				245					250					255	

Val	Arg	Ala	Lys	Gly	Ala	Gln	Xaa	Xaa	Xaa	Pro	Gly	Xaa	Xaa	Glu	Xaa
			260					265						270	

Xaa Xaa Gly Gln Gln Xaa Xaa Val Pro Xaa Xaa Xaa Xaa Leu Pro Ser
 275 280 285
 Xaa Pro Gln Xaa Xaa Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Xaa
 290 295 300
 Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His
 305 310 315 320
 Leu Ala Cys Leu Ser Pro Pro Leu Xaa Glu Ile Pro Ser Gly Xaa Trp
 325 330 335
 Arg Cys Ser Xaa Cys Leu Gln Xaa Xaa Val Gln Xaa Xaa Xaa Xaa Xaa
 340 345 350
 Xaa Glu Xaa Xaa Arg Pro Xaa Glu Xaa Pro Xaa Glu Thr Pro Xaa Xaa
 355 360 365
 Xaa Gly Leu Arg Ser Ala Xaa Glu Xaa Xaa Arg Gly Pro Xaa Xaa Glu
 370 375 380
 Xaa Xaa Ala Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Xaa Xaa Leu Xaa Ala
 385 390 395 400
 Pro Xaa Xaa Ala Ala Pro Leu Xaa Xaa Leu Xaa Xaa Ser Ala Leu Xaa
 405 410 415
 Pro Leu Leu Xaa Xaa Gly Xaa Glu Gly Xaa Xaa Xaa Xaa Ala Pro Xaa
 420 425 430
 Ala Arg Cys Xaa Val Cys Gly Asp Gly Thr Xaa Val Leu Arg Cys Xaa
 435 440 445
 His Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Xaa Xaa Xaa
 450 455 460
 Xaa Arg Pro Gly Thr Xaa Leu Arg Cys Xaa Ser Cys Ser Xaa Asp Xaa
 465 470 475 480
 Thr Pro Xaa Pro Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Ser Xaa Xaa
 485 490 495
 Arg Xaa Ala Pro Gly Xaa Ala Lys Xaa Xaa Asp Asp Xaa Ala Ser His
 500 505 510
 Xaa Pro Xaa Leu His Arg Asp Asp Leu Glu Ser Leu Leu Xaa Glu His
 515 520 525
 Xaa Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Xaa Arg Pro
 530 535 540
 Xaa Ala Xaa Xaa Pro Xaa
 545 550

<210> 11
 <211> 48
 <212> DNA
 <213> Mouse

<400> 11

ggggcctcga tggacgtctc tggggcccag gtcgtggttc gcgcgcta

48

<210> 12
 <211> 15
 <212> PRT
 <213> Mouse

<400> 12

Pro Glu Leu Pro Ala Glu Thr Pro Gly Pro Ala Pro Ser Ala Arg
 1 5 10 15

<210> 13
 <211> 43
 <212> DNA
 <213> Mouse

<400> 13
 agtgagcccc aggttaacca gaacgaggat gagtgtgccg tgt

43

<210> 14
 <211> 14
 <212> PRT
 <213> Mouse

<400> 14

Ser Glu Pro Gln Val Asn Gln Asn Glu Asp Glu Cys Ala Val
 1 5 10

<210> 15
 <211> 48
 <212> DNA
 <213> Mouse

<400> 15
 gtcaccaggc tcggttcctt cgggtcccat ctctactcgt ctttcacc

48

<210> 16
 <211> 15
 <212> PRT
 <213> Mouse

<400> 16

Val Val Arg Ala Lys Gly Ala Gln Gly Arg Asp Glu Gln Lys Val
 1 5 10 15

<210> 17
 <211> 20
 <212> DNA
 <213> Artificial sequence

<400> 17
 agaagtgcac ccagggtggc

20

<210> 18

<211> 20
 <212> DNA
 <213> Artificial sequence

<400> 18
 ggaagagggg cgtcagcaat

20

<210> 19
 <211> 15
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide

<400> 19

Met	Ala	Thr	Asp	Ala	Ala	Leu	Arg	Arg	Leu	Leu	Arg	Leu	His	Arg
1				5					10				15	

<210> 20
 <211> 14
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic peptide

<400> 20

Ser	Gln	Pro	Arg	Lys	Gly	Arg	Lys	Pro	Pro	Ala	Val	Pro	Lys
1				5					10				

<210> 21
 <211> 19
 <212> DNA
 <213> Artificial sequence

<220>
 <223> B127FR4-29 primer for PCR

<400> 21
 gctctggatg gcctactgc

19

<210> 22
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> B127FR4-17 primer for PCR

<400> 22
 agaagtgcac ccaggttggc

20

<210> 23
 <211> 19
 <212> DNA

<213> Artificial sequence

<220>

<223> B127FR4-33 primer for PCR

<400> 23

gtgtgctcgc tcagaaggg

19

<210> 24

<211> 18

<212> DNA

<213> Artificial sequence

<220>

<223> Forward primer Mforw4 for PCR

<400> 24

tggcaggtgg ggatggaa

18

<210> 25

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer Mrev15 for PCR

<400> 25

ggagggatgg aaggggagga

20

<210> 26

<211> 19

<212> DNA

<213> Artificial sequence

<220>

<223> Forward primer Mforw2 for PCR

<400> 26

tcccacctaagc agactaagc

19

<210> 27

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer Mrev32 for PCR

<400> 27

tcacagctct ctggacagaa

20

<210> 28

<211> 18

<212> DNA

<213> Artificial sequence

<220>
 <223> Primer B127FR4-21 for PCR

<400> 28
 ggcttctgag gctgcacc

18

<210> 29
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Double-paired finger motif

<400> 29

Cys Cys Cys Cys His Cys Cys Cys
 1 5

<210> 30
 <211> 42
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Structural motiff

<220>
 <221> VARIANT
 <222> (1)..(42)
 <223> Xaa is any amino acid

<400> 30

Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
 1 5 10 15

Xaa Xaa Xaa Xaa His Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
 35 40

CS
Conclude